

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/542,867
Source: PS
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/542,867

DATE: 02/02/2006
TIME: 11:41:17

Input Set : E:\401uspc.app.txt
Output Set: N:\CRF4\02022006\J542867.raw

3 <110> APPLICANT: Shinoda, Tetsuro
4 Itoyama, Kyō
5 Hamamura, Tetsuzo
8 <120> TITLE OF INVENTION: JUVENILE HORMONE ACID METHYLTRANSFERASE
9 GENES AND METHODS OF USING SAME
11 <130> FILE REFERENCE: 480230.401USPC
13 <140> CURRENT APPLICATION NUMBER: US 10/542,867
C--> 14 <141> CURRENT FILING DATE: 2005-07-20
16 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00415
17 <151> PRIOR FILING DATE: 2003-01-20
19 <160> NUMBER OF SEQ ID NOS: 38
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2890
25 <212> TYPE: DNA
26 <213> ORGANISM: Bombyx mori
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (125)..(961)
31 <223> OTHER INFORMATION:

W--> 33 <400> 1
34 aaaagactgt tcggcgatac cgcaagtgaga acagcgacac atcgcacgct ctttagttcaa 60
36 tacgaactta aaaaaaaaaa gtgcccacaa atattttatt gaaaaaaaaa atattaagtc 120
38 aaaa atg aac aat gca gat tta tac cgc aaa agt aac agc ctc caa aag 169
39 Met Asn Asn Ala Asp Leu Tyr Arg Lys Ser Asn Ser Leu Gln Lys
40 1 5 10 15
42 aga gat gct ctg cgc tgc ctc gag gaa cat gcg aat aag att aag tgg 217
43 Arg Asp Ala Leu Arg Cys Leu Glu Glu His Ala Asn Lys Ile Lys Trp
44 20 25 30
46 aaa aaa atc ggt gat aga gtc ata gat ttg ggt tgc gct gac ggt agt 265
47 Lys Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser
48 35 40 45
50 gtt act gat att ttg aaa gtt tac atg cca aaa aat tac gga aga tta 313
51 Val Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu
52 50 55 60
54 gtt ggc tgc gac ata agc gaa gaa atg gtg aaa tac gcg aat aaa cac 361
55 Val Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His
56 65 70 75
58 cac ggc ttc ggt agg act tcg ttc agg gtg ctc gac ata gag ggc gat 409
59 His Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp
60 80 85 90 95
62 ttg acc gca gac ctg aaa caa ggc ttt gat cac gtt ttc tct ttt tac 457
63 Leu Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr

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64	100	105	110	
66	acc ctc cac tgg atc aga gac cag gaa cga gct ttc cgg aac att ttc			505
67	Thr Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe			
68	115	120	125	
70	aat ctg ctt ggc gac gaa gga gat tgc tta ctt ctg ttc ctg ggc cac			553
71	Asn Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Phe Leu Gly His			
72	130	135	140	
74	act cct atc ttt gat gtt tac cgc aca ctc tcg cat aca gaa aaa tgg			601
75	Thr Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp			
76	145	150	155	
78	cat tct tgg ctc gag cac gtc gat cga ttt ata tca cct tac cat gac			649
79	His Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp			
80	160	165	170	175
82	aat gaa gat ccc gaa aaa gaa gtt aag aag ata atg gaa aga gtt gga			697
83	Asn Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly			
84	180	185	190	
86	ttt agc aat att gaa gtg caa tgc aaa acg ttg ttc tat gta tac gat			745
87	Phe Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp			
88	195	200	205	
90	gat ttg gat gtt tta aaa aaa tca gta gca gct atc aat cca ttt aat			793
91	Asp Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn			
92	210	215	220	
94	atc ccg aaa gac ata ctt gaa gac ttt tta gaa gat tac ata gat gta			841
95	Ile Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val			
96	225	230	235	
98	gta cgg gag atg agg ctg ctc gac agg tgt aat aac aat gtc ggt gaa			889
99	Val Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Val Gly Glu			
100	240	245	250	255
102	tca gtg tct ata aaa ttt aac tac aaa gtc atc agt gtt tac gcg aga			937
103	Ser Val Ser Ile Lys Phe Asn Tyr Lys Val Ile Ser Val Tyr Ala Arg			
104	260	265	270	
106	aaa tta tgt tta agt tta atg taa ttaagttaga aaaaaaaaaac aaatccgact			991
107	Lys Leu Cys Leu Ser Leu Met			
108	275			
110	tctaaatctt ggaaataagt ttttttaaca tatttctctc tctttgtctt cccagatttt			1051
112	cgtgattaag ctttcttattc actattttaa aaagctttct caatataattg aatacagttt			1111
114	agaatacagt tggtatctga aatcaactgat ttcaagtcg gttactttaga acaaatttaa			1171
116	ttagtttaatt gtatttataa ggaacgctac aatatttatt acagtaagta attttaaatt			1231
118	tccggaaaca gtggagttca gtggacaatg cagtatcagg agatggctta gatggatgga			1291
120	cgagctcaca gtcacccgggt gttaaagtggt tactggagcc catagacatc tacaatgtaa			1351
122	atgcccacac cgatatgagt tataaggctt cagaatagct gccccaccc tcaagccgaa			1411
124	acgcgttaact gcttcacggc agaaataggc agggcggtgg tacctacccg cgccgactta			1471
126	caagagctcc taccactagt gagagccagc tgctttttgt tgcgtgtaa aatcggtcgt			1531
128	tgtctctagt catatcatag ccgtacaaaa aaataagacaa cttgatatta taactgttct			1591
130	tcaaatttct cgtcacacat acgaaaataa agtttgatgt atttacccga aatataaatg			1651
132	ttaacatagc tcatacatac atacatataat aattcatata tacacattaa gtttaatac			1711
134	tctgaaatat gtctacccca aaacaagaaaa gcctactgta ctaaaattgt atgcagttt			1771
136	agtttaatg tattttta ataacagtga catotattag cgatacattg aactattca			1831
138	acacaacatt tttcatatta tttcctttg aatctaatta cttttttaa gccgcagtaa			1891

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140 gatggcggtg ttgtacgact taaagtgtt agaatttaaa ataattctt cggttggtaa 1951
142 attataattt aaatagaaaat ccatactatt ttaattactc aactcaacaa ctcaattatt 2011
144 ttttaaagga gatgtgtgag tgagcatcac tagagaattt tttgaccggtt gaccgattgg 2071
146 gctgatttct tttcattat atccgtaaat ttttaggacaa gttttgtacc accaactaca 2131
148 gccactacag tattcattga ttttaattt ccataagttt gttttgtgtt aagtatattt 2191
150 ataataacga taaatttggt ttgagtcgtg atagggttggac atttcaacta gtccgcttgc 2251
152 tcaatttggatt atactatgtg ctttagtgcgg gttctttac gctatcgaga acgttaaaga 2311
154 actcgcacta agcacactat ttttattttat ttgttgcaca aatataattt gaaacaatcg 2371
156 ttgtataatca tcattgttta aagtttcc tataaaatca taaacagtc aaaaattttat 2431
158 ttttagtggag aattacatga aacaaattt gaaacaaagt ttgatttatac ttcaatgt 2491
160 ttcatcttactg ttttaaagct taaggatataa aatggcatgt ttgtgtgtt actcaggccc 2551
162 taagcaacac gcgttggctt ttaagtaaac tttgaagtct tagttattcc tgggtttatt 2611
164 tggcacgttta gtaaaatcta ccctgccatt tagtaccatt agagtgcgaa tgattacagc 2671
166 gtatgattat ttgttacatt ttaattttt gttaattact taacgaaacc tgcccggtt 2731
168 ttattgacaa cataattttagt aaaacatgtg ataatttggaa caatgacaaa ttattgtt 2791
170 gtttaatttata ttcaattttt atataataat tgtaatgtg atgtttaat aaataaaaact 2851
172 aaagtgtaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaa 2890

175 <210> SEQ ID NO: 2

176 <211> LENGTH: 278

177 <212> TYPE: PRT

178 <213> ORGANISM: Bombyx mori

180 <400> SEQUENCE: 2

181 Met Asn Asn Ala Asp Leu Tyr Arg Lys Ser Asn Ser Leu Gln Lys Arg.
182 1 5 10 15
184 Asp Ala Leu Arg Cys Leu Glu Glu His Ala Asn Lys Ile Lys Trp Lys
185 20 25 30
187 Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser Val
188 35 40 45
190 Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu Val
191 50 55 60
193 Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His His
194 65 70 75 80
196 Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp Leu
197 85 90 95
199 Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr Thr
200 100 105 110
202 Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe Asn
203 115 120 125
205 Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Leu Phe Leu Gly His Thr
206 130 135 140
208 Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp His
209 145 150 155 160
211 Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp Asn
212 165 170 175
214 Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly Phe
215 180 185 190
217 Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp Asp
218 195 200 205
220 Leu Asp Val Leu Lys Ser Val Ala Ala Ile Asn Pro Phe Asn Ile

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Output Set: N:\CRF4\02022006\J542867.raw

221	210	215	220	
223	Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val Val			
224	225	230	235	240
226	Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu Ser			
227	245	250	255	
229	Val Ser Ile Lys Phe Asn Tyr Lys Val Ile Ser Val Tyr Ala Arg Lys			
230	260	265	270	
232	Leu Cys Leu Ser Leu Met			
233	275			
236	<210> SEQ ID NO: 3			
237	<211> LENGTH: 938			
238	<212> TYPE: DNA			
239	<213> ORGANISM: Drosophila melanogaster			
241	<220> FEATURE:			
242	<221> NAME/KEY: CDS			
243	<222> LOCATION: (1)..(894)			
244	<223> OTHER INFORMATION:			
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247	atg aat cag gcc tct cta tat cag cac gcc aac cag gtg caa agg cac			48
248	Met Asn Gln Ala Ser Leu Tyr Gln His Ala Asn Gln Val Gln Arg His			
249	1 5 10 15			
251	gat gcc aaa ttg att ctg gat gag ttc gca tcg acc atg cag tgg cga			96
252	Asp Ala Lys Leu Ile Leu Asp Glu Phe Ala Ser Thr Met Gln Trp Arg			
253	20 25 30			
255	tcc gat gga gag gat gcc ctc ctg gat gtg ggt tca gga tct ggt aac			144
256	Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn			
257	35 40 45			
259	gtg ctc atg gac ttt gta aag cca ctg ctc ccg att cgt gga caa ctg			192
260	Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu			
261	50 55 60			
263	gtg ggc aca gac atc tcc agc cag atg gtg cac tat gcc agt aag cat			240
264	Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His			
265	65 70 75 80			
267	tac cag cga gag gag cgt acc aga ttc oag gtt ctg gac att gga tgc			288
268	Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys			
269	85 90 95			
271	gaa cgg ctg ccc gag gag ctg agc ggc aga ttt gac cat gtc acc tcg			336
272	Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser			
273	100 105 110			
275	ttc tac tgc ctc cat tgg gtg caa aat ctg aaa gga gct ctc gga aat			384
276	Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn			
277	115 120 125			
279	atc tac aat ctt ctg aag ccc gaa ggt ggc gac tgc ctc ctg gca ttt			432
280	Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe			
281	130 135 140			
283	ttg gcc tcc aat ccg gtt tac gaa gtc tat aag att ctt aaa acg aat			480
284	Leu Ala Ser Asn Pro Val Tyr Glu Val Tyr Lys Ile Leu Lys Thr Asn			
285	145 150 155 160			
287	gac aag tgg tcg act tat atg cag gat gtg gag aac ttc ata tcc cca			528

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288	Asp	Lys	Trp	Ser	Thr	Tyr	Met	Gln	Asp	Val	Glu	Asn	Phe	Ile	Ser	Pro	
289							165			170					175		
291	ctt	cac	tac	agt	cta	aat	cct	ggc	gag	gaa	ttc	agc	cag	ttg	ttg	aac	576
292	Leu	His	Tyr	Ser	Leu	Asn	Pro	Gly	Glu	Glu	Phe	Ser	Gln	Leu	Leu	Asn	
293							180			185				190			
295	gat	gtg	ggt	ttc	gtg	caa	cac	aat	gtg	gaa	att	cga	aac	gaa	gtg	ttt	
296	Asp	Val	Gly	Phe	Val	Gln	His	Asn	Val	Glu	Ile	Arg	Asn	Glu	Val	Phe	624
297							195			200				205			
299	gtt	tat	gaa	ggt	gta	agg	act	ctg	aaa	gat	aat	gta	aag	gcc	att	tgt	672
300	Val	Tyr	Glu	Gly	Val	Arg	Thr	Leu	Lys	Asp	Asn	Val	Lys	Ala	Ile	Cys	
301							210			215				220			
303	cct	ttt	ctt	gag	cga	atg	cct	gca	gat	ttg	cat	gaa	cag	ttc	ctg	gat	720
304	Pro	Phe	Leu	Glu	Arg	Met	Pro	Ala	Asp	Leu	His	Glu	Gln	Phe	Leu	Asp	
305							225			230				235		240	
307	gac	ttc	ata	gac	att	gtt	ata	tcc	atg	aat	ttg	cag	caa	ggt	gaa	aat	
308	Asp	Phe	Ile	Asp	Ile	Val	Ile	Ser	Met	Asn	Leu	Gln	Gln	Gly	Glu	Asn	768
309							245			250				255			
311	aat	gag	gat	caa	aag	ttc	cta	tct	ccc	tat	aaa	ctg	gtg	gtg	gcc	tat	
312	Asn	Glu	Asp	Gln	Lys	Phe	Leu	Ser	Pro	Tyr	Lys	Leu	Val	Val	Ala	Tyr	
313							260			265				270			
315	gct	cgc	aag	act	cct	gaa	ttt	gtg	aat	aat	gtt	ttc	ctg	gag	cct	aca	864
316	Ala	Arg	Lys	Thr	Pro	Glu	Phe	Val	Asn	Asn	Val	Phe	Leu	Glu	Pro	Thr	
317							275			280				285			
319	cat	caa	aac	ttg	gtt	aag	gga	ata	aat	taa	ttttatTTta	caaattaaca				914	
320	His	Gln	Asn	Leu	Val	Lys	Gly	Ile	Asn								
321							290			295							
323	gtaattgcat	ttgttaacag	agtc													938	
326	<210>	SEQ	ID	NO:	4												
327	<211>	LENGTH:	297														
328	<212>	TYPE:	PRT														
329	<213>	ORGANISM:	Drosophila	melanogaster													
331	<400>	SEQUENCE:	4														
332	Met	Asn	Gln	Ala	Ser	Leu	Tyr	Gln	His	Ala	Asn	Gln	Val	Gln	Arg	His	
333	1					5				10				15			
335	Asp	Ala	Lys	Leu	Ile	Leu	Asp	Glu	Phe	Ala	Ser	Thr	Met	Gln	Trp	Arg	
336						20				25				30			
338	Ser	Asp	Gly	Glu	Asp	Ala	Leu	Leu	Asp	Val	Gly	Ser	Gly	Ser	Gly	Asn	
339						35				40				45			
341	Val	Leu	Met	Asp	Phe	Val	Lys	Pro	Leu	Leu	Pro	Ile	Arg	Gly	Gln	Leu	
342						50				55				60			
344	Val	Gly	Thr	Asp	Ile	Ser	Ser	Gln	Met	Val	His	Tyr	Ala	Ser	Lys	His	
345						65				70				75		80	
347	Tyr	Gln	Arg	Glu	Glu	Arg	Thr	Arg	Phe	Gln	Val	Leu	Asp	Ile	Gly	Cys	
348						85				90				95			
350	Glu	Arg	Leu	Pro	Glu	Glu	Leu	Ser	Gly	Arg	Phe	Asp	His	Val	Thr	Ser	
351						100				105				110			
353	Phe	Tyr	Cys	Leu	His	Trp	Val	Gln	Asn	Leu	Lys	Gly	Ala	Leu	Gly	Asn	
354						115				120				125			
356	Ile	Tyr	Asn	Leu	Leu	Lys	Pro	Glu	Gly	Gly	Asp	Cys	Leu	Leu	Ala	Phe	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; N Pos. 6,15
Seq#:20; N Pos. 6,12
Seq#:29; Xaa Pos. 2,3,5,7
Seq#:30; Xaa Pos. 5,8,9,13
Seq#:31; Xaa Pos. 1,4
Seq#:32; Xaa Pos. 1,3,10
Seq#:33; Xaa Pos. 9
Seq#:34; Xaa Pos. 2,5,8
Seq#:35; Xaa Pos. 4
Seq#:36; Xaa Pos. 4

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34
Seq#:35,36

VERIFICATION SUMMARY
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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:31
L:246 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:244
L:400 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:398
L:545 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:543
L:695 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:693
L:957 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:1140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:1194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:1212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:1258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:1276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0